

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.

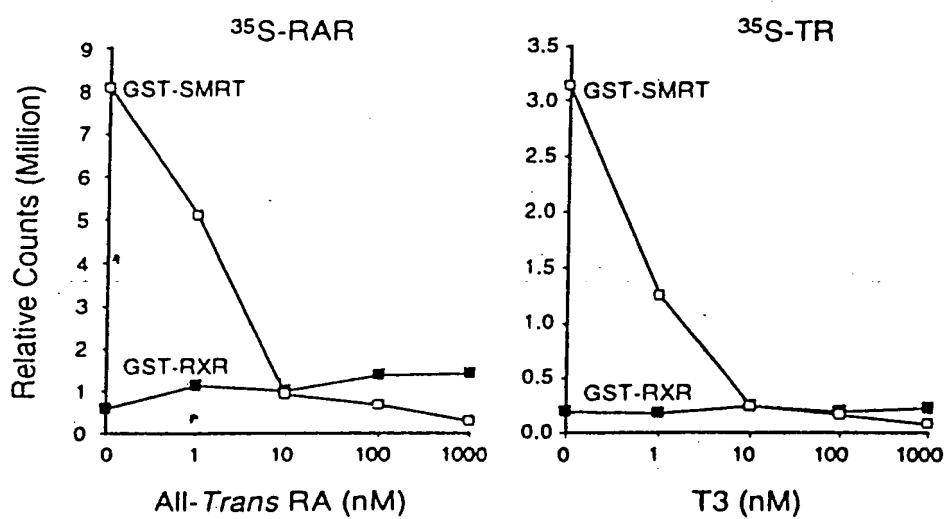


FIGURE 1



1 MEAWDAH~~D~~KEAFAAAEAQKL~~D~~G~~D~~DCWTSGL~~D~~F~~D~~V~~D~~REVIKAS~~D~~HA~~D~~
51 SAFSYA~~D~~EGH~~D~~BL~~D~~GLHDTAR~~D~~V~~D~~LER~~D~~ITISNE~~D~~PLISSAKH~~D~~SVLERQI
101 GAI~~D~~SQGMSVQLHV~~D~~Y~~D~~SEHAKA~~D~~V~~D~~GT~~D~~VMGL~~D~~BL~~D~~MD~~D~~OKKLA~~D~~FSGVKQEQL
151 SPRGQAGPPESLGVPTAQEA~~D~~VLRGTALGSVP~~D~~GG~~D~~ITKGIPSTRVPSDSA
201 ITYRGSITHGTPADVLYKG~~D~~TITRI~~D~~IGEDPSRLDRGRED~~D~~SLPKGHVIYEG
251 KKGVLSYEGGMSVTQCSKEDGRSSGPPHETA~~D~~APKRTYDMMEGRVGRAI
301 SSASIEGLMGRAIPPERHSPHLKEQHHIRGSITQGIPRSYVEAQEDYLR
351 REAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKLKP~~D~~AHEGLVATVKEAG
401 RSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHD
451 VRS~~D~~LIGSPGRTFPPVHPLDV~~D~~MADARALERACEESLKSRPGTASSGGSI
501 AR~~D~~GA~~D~~PVIVPELGKPRQSPLTYEDHGAPFAGH~~D~~LPRGSPVTMREPTPRLQEG
551 SLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPIS~~D~~PYEHLLRGVSGVD
601 LYRSHIPLAFDPTSIPRG~~D~~IPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRG
651 YPD~~D~~TAALENRTQIINDYITSQQMHNTATAMAQRADMLRGLSPRESSLAL
701 NYAAGPRGIIDL~~D~~SQVPHLPVLVPP~~D~~PG~~D~~TPATAMDRLAYLPTAPQPFSSRH
751 SSSPLSPGGPTH~~D~~LT~~D~~KPTTSSSERERDRDRER~~D~~REREKSILTSTTTVE
801 HAPIWRPGTEQ~~D~~SSGSSGGGGSSSRPASHSHAHQHSPIS~~D~~RTQDALQ
851 QRPSVLHNTGMKG~~D~~IITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLG
901 GTLDGVYPTLMEPVLLPKEAPRVARPERP~~D~~ADTGHAF~~D~~LA~~D~~KPPARSGLEPA
951 SSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASADPH
1001 REKTQSKPFSI~~D~~QELELRL~~D~~SLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPK
1051 HLEELDKSHLEGELRPKQPGPV~~D~~KLGGEAHLPHLRPLPES~~D~~QSSSPLL~~D~~ C-SMRT
1101 APGVKG~~D~~RVVTLA~~D~~HISEVIT~~D~~DYTRHH~~D~~LSAPL~~D~~PAPLYS~~D~~PGASCP
1151 VLDLRRPPSDLYL~~D~~PPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGI
1201 EPVSPPEGMTEPGHSRS~~D~~AVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFF

1251 SK~~D~~TESNSAM~~D~~KS~~D~~KKQ~~D~~E~~D~~INKKLNT~~D~~NRNEPEYNISQPGTEIFNMPAITGT

1301 GL~~D~~TYRSQA~~D~~QEHASTNMGLEAIIRKALM~~D~~KYDQW. EESPPLSANAFNPL

1350 NASASLPAAMPITAADGRSDHTLTSP~~D~~. GGGGAKVSGR~~D~~SSRKAKSPAPG

1399 LA. . SGDRPPSVSSVHSEGDCNRR~~D~~PLTNRVWEDRPSSAGSTPFPYNPL~~D~~

1447 MRLQAG~~D~~MAS~~D~~PPPG~~D~~PAGSGP~~D~~. . AGPHHA. . WDEEPKPL~~D~~CSQYET~~D~~



FIGURE 3A

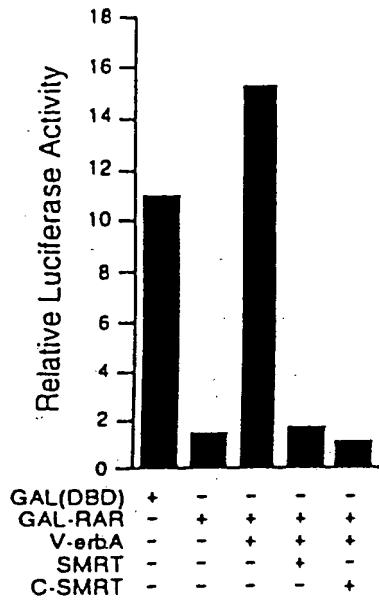


FIGURE 3B

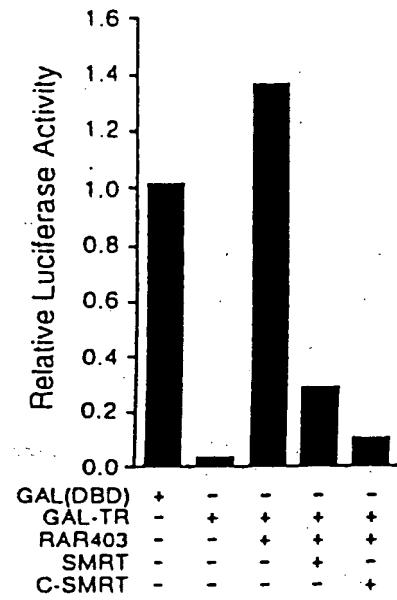


FIGURE 3C

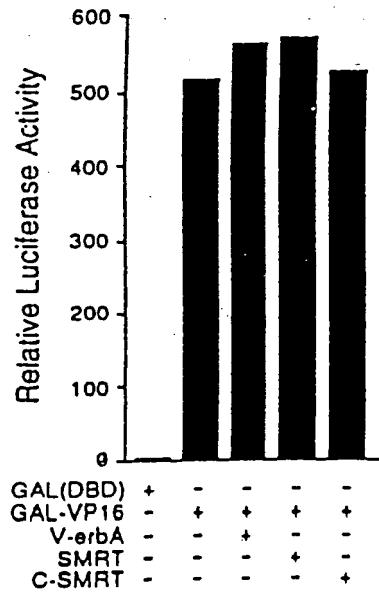
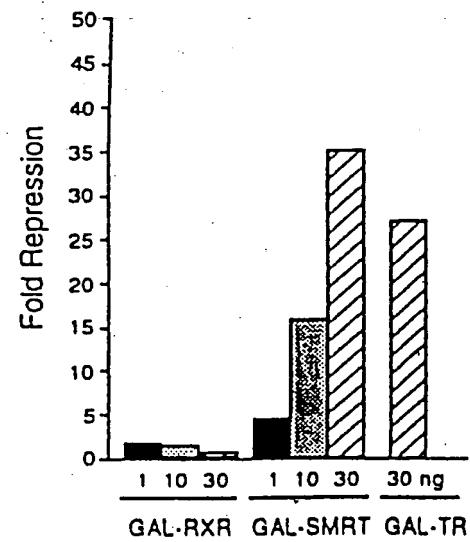


FIGURE 3D





MSGSTQVLVAQTWRATEPRYPPHSLSYPPVQIARTHTDVLLEYQHHSRDYASHLSPGSIIQPPQRRRPSLSEFQPGNERSQELHLRPEHSYLPPELGKSEM
MSGSTQPVQATWRRAEPRYPPHGISYPPVQIARSHDVLLEYQHHPDVTSHLSPGSIIQPPQRRRPSLSEFQPGSERSQELHLRPESTFLPELGKPD
101 EFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLTKDRSLTGKLEPVSPSPHTDPELELVPPRLSKEELIQLNMDRVDRITMVEQQQISKLKKKQQQL
101 EFTESKRPRLELLPDPLLRPSPLLATGQPSGSEDLTKDRSLAGKLEPVSPSPSPHADPELELAPSRLSKEELIQLNMDRVDRITMVEQQQISKLKKKQQQL
201 EEEAAKPPPEKEPKVSPPPPIESKHLRSLVQIYDENRKKAEEAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHRKQWKQPCQ
201 EEEAAKPPPEKEPKVSPPPPIESKHLRSLVQIYDENRKKAEEAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHRKQWEQRFQ
301 RYDQLMEEALKVERIENNRRRAKESKVREYYEKQFPEIRKQRELQERMQSRVGQRGSGLMSMAARSEHEVSEIIIDGLSEQENLEKQMRQLAVIPPMY
301 RYDQLMEEALKVERIENNRRRAKESKVREYYEKQFPEIRKQRELQERMQSRVGQRGSGLMSMAARSEHEVSEIIIDGLSEQENLEKQMRQLAVIPPMY
401 DADQRIKFINMNGLMADPMKVYKDRQVMNWSEQEKETFRKFMQHPKNGLIAASFLERKTVACVLYYLTKNNENYKSLVRRSYRRRGKSQQQQQQQ
401 DADQRIKFINMNGLMDDPMKVYKDRQVMNWSEQERDTFRKFMQHPKNGLIAASFLERKTVACVLYYLTKNNENYKSLVRRSYRRRGKSQQQQQQQ
501 QQQQQQQQQPMPRSSQEEKDEKEKEKEAEEKEEKPEVENDKEDELLKEKTDTSGEDNDEKEAVASKGRKTANSQGRKGRITRSMANEANSEEATPQQ
501 QQQQQQQ---MARSSQEEKDEKEKEKEADKEEKAQDAENEKEELSKETDTSGEDNHEKEAVASKGRKTANSQGRKGRITRSMANEANHEETATPQQ
601 SAE LASMELNESSRWTEEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCQKNFYFNYKQRQLNDEILQHQLKLMKERNARRKKKAPAAASEEEAAPPVV
597 SSELASMELNESSRWTEEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCQKNFYFNYKQRQLNDEILQHQLKLMKERNARRKKKTPAAASEETAFPPVA
701 EDEEMEASGVSGNEEEEMVEAEALHASGNEVPR-GECSGPATVNNSSDTEIPSHTEAAKDTGQNGPKPATLGADGPPGPPTPRRTSRAPIEPTPA
697 EDEEMEASGASANEEELAEEAQSAGNEVPRVGECSGPAAVNNSSDTEVSPSPRSEAMKDTG---PKPTGTEALPAATQPPVPPPEEPAVAPAEPPSV
800 SEATGAPTPPPAPPSPSAPPVVPKEEKEETAAAPP--VEEGEEQKPPAEE-LAVDTGKAEEP--VKSECTEEAEEGPA-KGKDAEAAEATAEGALK
794 PDASGPPSPPSHLPH-PRLLWTRMNKKPRLQLPQRMPRSRSLSRPRRSMSWEKPEEPEASEEPPESEVSKSDHKEETEEPEPDKAKGTEAIETVSEAPLK
893 AEKKEGGSGRATTAKSSGAPQDSDSATCSADEVDEAEGGDKNRLLSPRSPSLTPTGDRPANASPKPLDLKQLKQRAAIPIQVTKVHEPPREDAAPT
893 VEE-AGSKAAVTKGSSGATQDSDFSATCSADEVDEPEGGDKGRLLSPRSPSLTPTAGDPRASTSPQKPLDLKQLKQRAAIPIQVTKVHEPPREDTVPP
993 KAPPAPPAPPQNLPQESDAPQPGSSPRGKSRSPAPPADKEA-----FAAAEAQKLPDPCTSGLPFPVPPREVIKASPHADPSAFSYAPPGHPL
992 KPVPPVPPPTQHLQPEGDVSQSGGSPRGKSRSPVPPAEEAKPAFFPATEGPKLPTEPPRWSGLPFPPIPPEVIKTSPHAADPSAFSYTPPGHPL
1095 PLGLHDTARPVLPRPTISNPPLISSAKHPSVLERQIGAISQ-GMSVQLHVPSHAKAPVGPVTMGLPLPMDPKLAPPSGVKQEQLSPRGQAGPPES
1092 PLGLHDSARPVLPRPISNPPLISSAKHPSVLERQIGAISQGMSVQLRVPHSEHAKAPMGPLTMGLPLAVDPKKL-----
1184 LGVPTAQEASVLRGTAALGSVPGGSITKGIPSTRVPSDASITYRGSITHGTPADVLYKGTITRIIGEDSPSRDLRGREDSLPKGHVIEGKKGHVLSEYGG
1169 -----GTALGSATGSITKGIPSTRADGPS--YRGSITHGTPADVLYKGTISRIVGEDSPSRDLRAREDTLPKGHVIEGKKGHVLSEYGG
1284 MSVTQCSKEDGRSSSGPHEATAKRTYDMMGRVGRAISSASIEGLMRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRRREAKLLKREGT h-SMRT
1254 MSVSQCSKEDGRSSSGPHEATAKRTYDMMGRVGRVTVSASIEGLMRAIP-EQHSPH-LKEQHHIRGSITQGIPRSYVEAQEDYLRRREAKLLKREGT m-SMRT
1384 PPPPPPSRDLTEAYKT---QALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITOQGTPKLKYDTGASTTGSKKHDVRSILIGSP h-SMRT
1352 PPPPPPPRDLTETYKPRPLDPLGPKLKPHTHEGVVATVKEAGRSIHEIPREELRRTPELPLAPRPLKEGSITOQGTPKLKYDGSAPSTGKHDVRSIIGSP m-SMRT
1481 GRTFPVHPLDVMADARALERACYEESLKSRSRGTAASSGGSIARGAPVIVPELPGKPRQSPPLTYEDHGAPFAGHLPGRGSPVTMREPTPRLQEGSSLSSKAS h-SMRT
1452 GRPPPAHLPLDIMADARALERACYEESLKSRSGTSSGAGGSITRGAPVVVPELPGKPRQSPPLTYEDHGAPFTSHLPRGSPVTTREPTPRLQEGSSLSSKAS m-SMRT
1581 QDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPIRGIPILDAAA---YLYPRHLAPNPTYPHYPPYLIRGYPDTAAL h-SMRT
1552 QDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLLRGVTGVDLYRGIPLAFDPTSIPIRGIPLEAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL m-SMRT
1690 ENRQTIINDYITSQQMHHTATAMAQRADMRLGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSPLSP h-SMRT
1652 ENRQTIINDYITSQQMHNAASAMAQRADMRLGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAIDRLAYLPTAPQPFSSRHSSPLSP m-SMRT
1780 GGPHTLKPPTTSSSERERDRDRERDRREREKSILSTTTVHEAPIWRPGTEQSSGSSGGGGSSSRPASHSHAHQHSPISRTQDALQQRPSVLU h-SMRT
1752 GGPHTLAKPTATSSSERERERERD-----KSILSTTTVHEAPIWRPGTEQSSGAGGSS-----RPASHTHQH-SPISRTQDALQQRPSVLU m-SMRT
1680 NTGMKGIIATAVEPSKPTVLR---STSTSSPVRAATFPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADEGHAFLAKPPARSGLEPASSPS h-SMRT
1836 NTSMKGVVTSEPGPTVLRWARSTSTSPVRAATFPATHCPLGGTLEGVYPTLMEPVLLPKETSRSRVARPERARVDAHAFPLKPPGR---EPASSPS m-SMRT
1977 KGSEPRPLVPPVSGHATIARTPAKNLAPHASPDPPAPPASADPHREKTSQKPPSIQELELRLSLGYH-GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE h-SMRT
1933 KSSEPRSLAPPSSHTAIARTPAKNLAPHASPDPPAPT-SASDLHREKTSQKPPSIQELELRLSLGYHSGAGYSPDGVEPISPVSSPSLTHDKGLSKPLE m-SMRT
2076 ELDKSHLEGELRLPKQPGPVKLGGEAAHPLHLRPLPESQPSPLLQTAGPVGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAFLYSPFGASCPCVLD h-SMRT
2032 ELEKSHLEGELRLHQPGPMKLSAEEAHLPHLRLPESQPSPLLQTAGPGIKGHQRVVTLAQHISEVITQDYTRHHPQQLSGPLPAFLYSPFGASCPCVLD m-SMRT
2176 LRRPPSDLYLPPPDHGAPARGSPHSSEGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRGMGSKSPGNTSQPPAFFSKL h-SMRT
2132 LRRPPSDLYLPPPDHGTPARGSPHSSEGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPPGNTSQPPTFFSKL m-SMRT
2276 TESNSAMVSKKQEIINKLNTHNRNEPEYNIISQPGTEIPNMPAITGTGLMTYRSQAVQEHASTNMGLAIIIRKALMGKYDQWEESPPLSANAFLNANA h-SMRT
2231 TESNSAMVSKKQEIINKLNTHNRNEPEYNIQPGTEIPNMPAITGAGLMTCSRQAVQEHASTNMGLAIIIRKALMGKYDQWEFPPLGANAFLNANA m-SMRT
2376 SLPAA-MPITAADGRSDHTLTSPPGGGKAKVSGRPSRKAKSPAPGLASGRDRPPSVSSVHSEGDNCNRRPLTNRVWEDRPPSAGSTPFPYNPLIMRLQAG h-SMRT
2331 SLPAAAMPITTADGRSDHALTSPPGGGKAKVSGRPSRKAKSPAPGLASGRDRPPSVSSVHSEGDNCNRRPLTNRVWEDRPPSAGSTPFPYNPLIMRLQAG m-SMRT
2475 VMASPPPPGLPAGSGPLAGPHHAWDEEPKPLLCQSQYETLSDSE h-SMRT
2431 VMASPPPPGLAAGSGPLAGPHHAWDEEPKPLLCQSQYETLSDSE m-SMRT

FIGURE 4



A FAMILY OF TRANSCRIPTIONAL CO-REPRESSORS THAT
INTERACT WITH NUCLEAR HORMONE RECEPTORS AND USES
THEREFOR - Evans et al. - 09/522,753 - Sheet 5 of 13

JAN 26 2004

FIGURE 5A

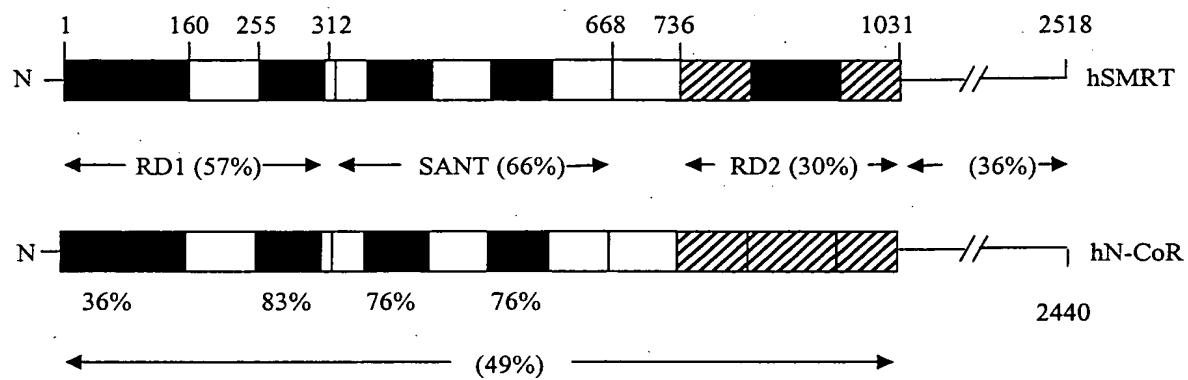


FIGURE 5B



FIGURE 6A

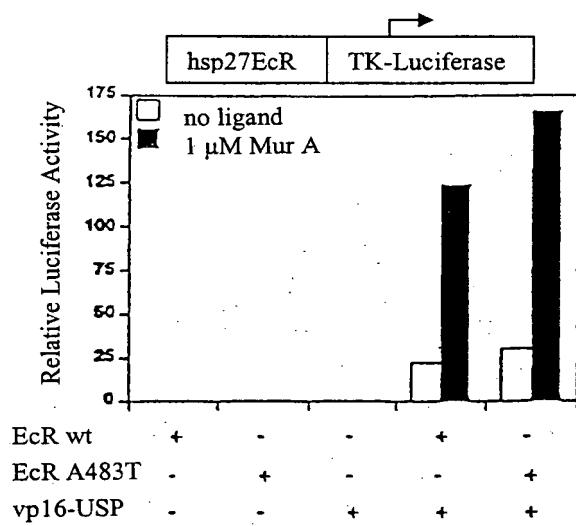


FIGURE 6B

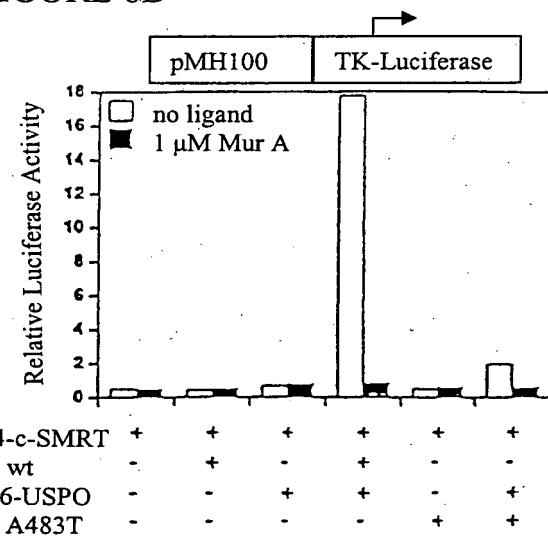
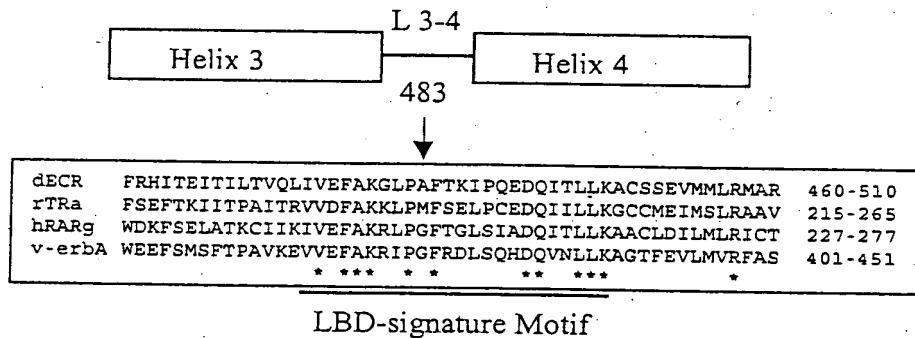


FIGURE 6C



JAN 26 2004

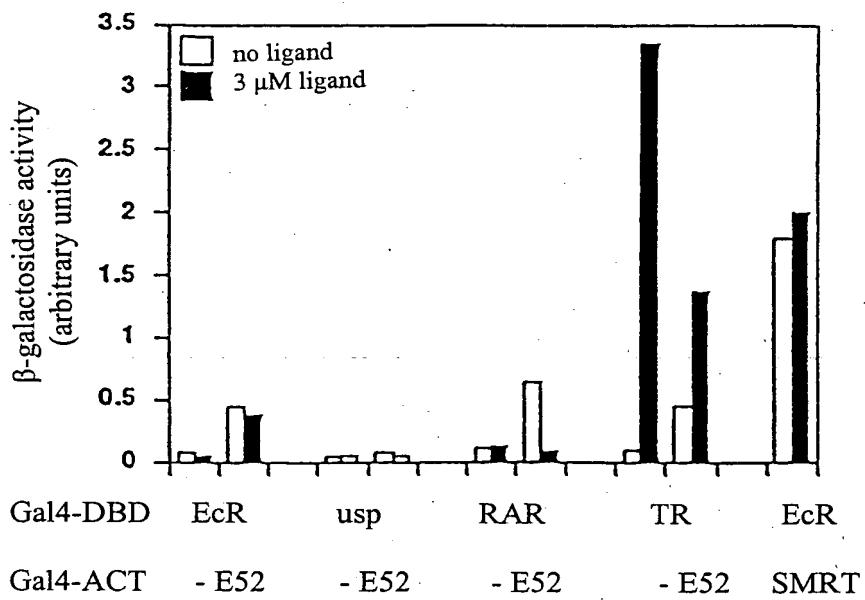


FIGURE 7



FIGURE 8A

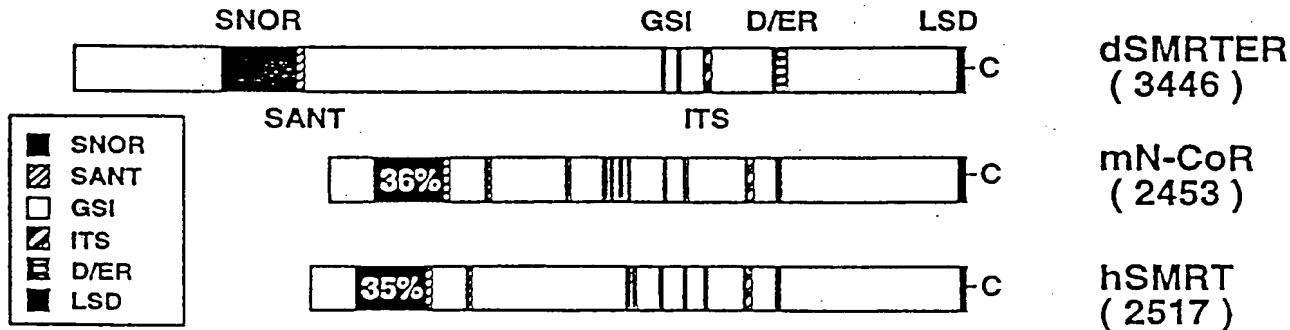


FIGURE 8B

JAN 26 2004

OFFICE 9203

SNOR motif

SMRTER : 573
mN - CoR : 177
hSMRT : 169

10	20	30	40	50
KEELLMLQIQKVVDNEITKSAETTMETLIRKKEKSLMEEAALAK	KEELIQSMDRVDRERIAKVEQQIILKLLKKQQLEEEA- -AKP	KEELIQNMDRVDRERITMVEQQIISKLLKKQQLEEEA- -AKP	PEAKEQRAAKELNDPEPEKPVSPPEPEKPVSP	PEAKEQRAAKELNDPEPEKPVSPPEPEKPVSP

SMRTER: 623
mN-CoR: 226
hSMRT: 217

60 70 80 90 100

```

NNNDQEPMVELSWRSQMIAEKIVAANRKTAPCHSMLIONAAADESSSPGSV
-----PFVEQKHRS-----IVQIIYDENRKKAAEAHKIFEGLGPKVE-----
-----PPIESKHRS-----LVQIIYDENRKKAAEAHRILEGLGPOVE-----

```

SMRTER: 673
mN-CoR: 263
hSMRT: 254

110	120	130	140	150
AGRPWLPPLYNQHLDVEALAMLIROHOSQIRAPILLHIRKLKAERWAHNG				
-----LPLYNQPSDTKVNHENIKINQV-MRKKLILEFKRRNHARKQREQK				
-----LPLYNQPSDTROYHENIKINQV-MRKKLILYFKRRNHARKQWQK				

SMRTER: 723
mN-COR: 307
hSMRT: 298

160 170 180 190 200
I V E K Y T K D Q A D W Q R R I C E R M E A S A K R K A E K N R E F F E K V F I E L R K Q R E D K
I C Q R Y D Q L M E A W E K K V D R I E N N P R R K A K E S K T R E Y Y E K Q F P E I R K Q R E Q Q
F C Q R Y D Q L M E A L E K K V E R I E N N P R R K A K E S K V R E Y Y E K Q F P E I R K Q R E Q Q

SMRTER : 773
mN-COR : 357
hSMRT : 348

	210	220	230	240	250	
ERFN	RVGSR	IKSEADLEE	IMDGLOQE	QALED	KKMR	SYAVIP
ERFO	RVGQORGAGL	SATIARSEHEI	SEI	IDGLSEQEN	NEKOMR	OLSNIP
ERM	DSRVGQRG	SGLSMSAARSEHEV	SEI	IDGLSEQEN	LEKOMR	OLAVIP

SMRTER : 814
mN-CoR : 406
hSMRT : 398

260 270 280
LMHDADORRRCAYHNENGLIEDMVAVHQQRKALNM
MMFDADAEORRVKFINMNGLAMEDPMKVKYKDRQFMNV
MLYDADOOQRIKFINMNGLMAADPMKVKYKDRQVMNM

SANT domain

SMRTER	: 848	WTAGEKETFKEKYLOHFKNFGATIASSLDR	KSPODCVRYYYLSKKTENY	100%
mN-CoR(1)	: 440	WTIDHEKEIIFKDKFIOHPKNFGLIASYLER	KSVPDCVLYYYLTKKNENY	68/80%
hSMRT(1)	: 432	WSEOEKETFREKFPMOHPKNFGLIASPLER	KTVAECLVLYYYLTKKNENY	64/82%
c14B9.6	: 615	WSPEERSLFKSRROADHMKIFHGLTEEFVD	KTASDILVLFYYMNNKKTEDY	35/53%
cF53H10	: 218	WTPDEIYOFODAIYQSEKDFDKVAVELPG	-KSVKECVQFYTWKKDCPD	38/56%
xER1	: 277	WTEEECRNFEQGLKAIKGKDFHLIQANKVRLRSVGECVAFYYMWKKSERM		36/56%
mN-CoR(2)	: 627	WTEEEEMEVAKKGVLVEHGRNWAAIAK-MVGT	KSEAOCKNFYFNYKRRHNL	34/53%
hSMRT(2)	: 615	WTEEEEMETAKKGLLEHGRNWSAIAAR-MVGS	NTVSQCKNFYFNYKKRQNL	38/57%
hKIAA0071	: 106	WTIVDKVLFEOAFSFHRIQOMLPD	-KSIASLVKFYYSWKKERTK	37/50%
CMTA-I	: 198	WTDEOEITLFLENCYQIFGKNSQIR	-RSLOSSIVOFYYEISKRKVKY	39/51%
YCR592	: 673	FTDHEHSLFEGVILTHEKCKP		

ITS motif

SMRTER : 2424 TRQIVMHDYITSQQM
SMRT : 1681 NROTHINDYITSQQM
N-COR : 1615 TRQITLNDYITSQQM

CSI motif

MRTER: 2274 VKSGSIHGT PANS
 2236 GKHGSITQGTPLHM
 SMRT: 1203 VPGGSITKCFPSTR

N₂CO₃

LSD motif

SMRTER : 34300 ESKPLLLSKYDALSDE
SMRT : 2501 EFKPLLCSCSYETLSDSEL
N-COR : 2436 EPAPILISAGYETLSDSEL

C14B9-6:

MRTER:	2 2 7 4	V K S G S I L H G T P A N S
	2 2 3 6	G K H G S I T Q G T P L H M
SMRT:	1 2 0 3	V P G G S I T K G I P S T R
	1 2 2 4	T Y R G S I T H G T P A D V
	1 3 5 0	H I R G S I T Q G I P R S Y
	1 4 4 6	L K E G S I T Q G T P L K Y
	1 5 1 7	S S G G S I A R G A P V I V
N-COR:	9 2 1	T P P G S I L I S S P I K P
	1 0 6 4	I M G G S I S Q G T P G T Y
	1 0 9 2	P S V G S I S L G I P R Q Q
	1 1 4 9	V Q E G S I T R G T P A S K
	1 1 7 1	S L R G S I T Q G T P A L P
	1 3 0 2	V L S G S I M Q G T P R A T
	1 3 8 8	I I E G S I S Q G T P I K F
B9 6:	8 2 0	O T G S I S E C T P R O

FIGURE 9

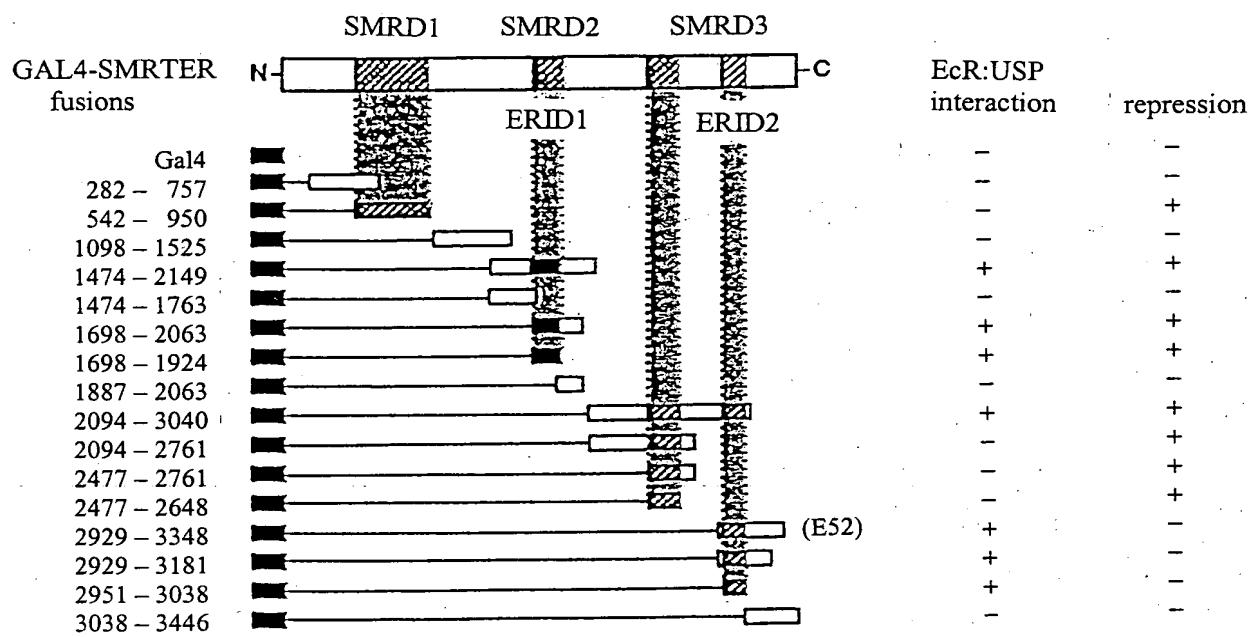


FIGURE 10



FIGURE 11A

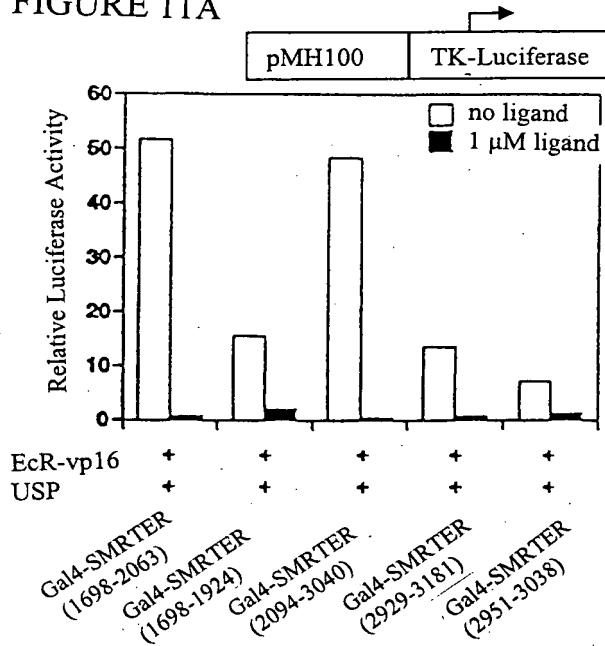


FIGURE 11B

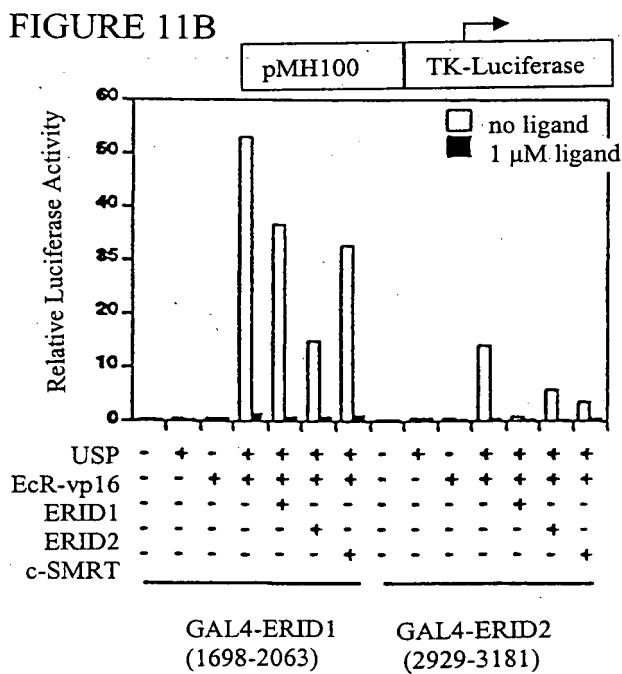


FIGURE 11C

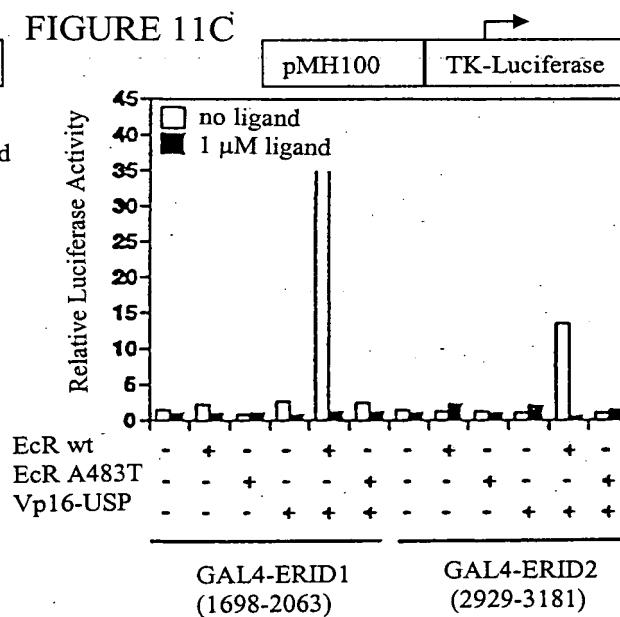




FIGURE 12A

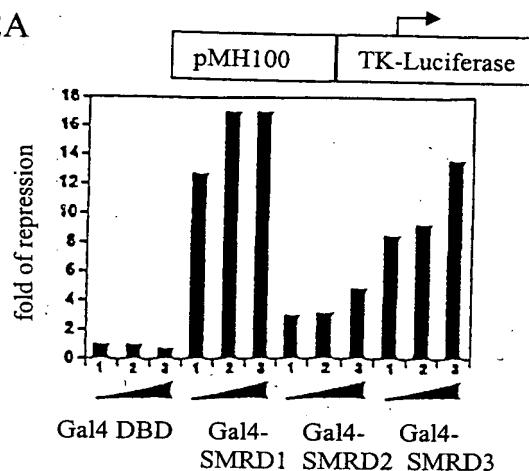


FIGURE 12B

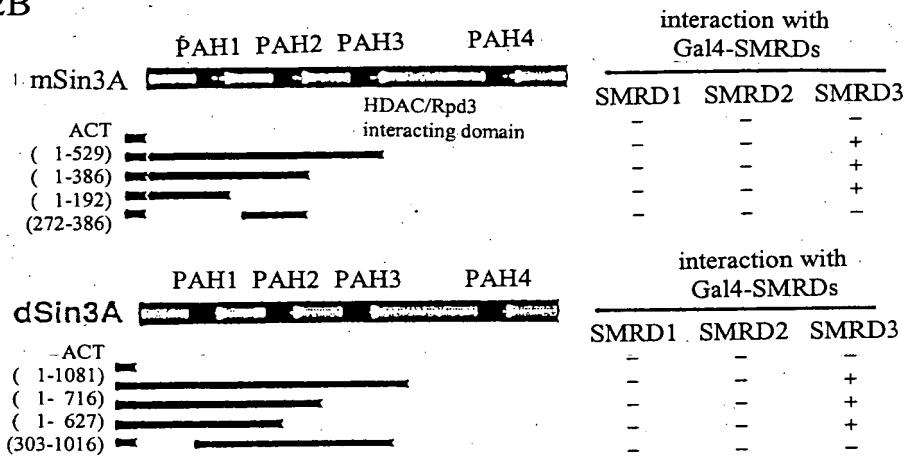


FIGURE 12C

